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BP 191 sloós EVRY codex - France
Email: sequef quenoscope.cus.ft, Web : WWW.genoshope.rus.ft.
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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| National Institutes of Health, Mammalian Gene Collection (MGC)
                   123 isTyrTrpSerGluAsnLeuPheClnCysPheAsnCysSerLeuCysLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                  156 rCysHisAlaGlvPhePheLeuAraGluAsnGluCysValSerCysSerA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 SerCysSerLysCysArqLysCluMetClyClnValClulleSerSerCy 106
                                                                                                                                                                                                                                493 AGCIGCICCAAAIGTOGAAAAGAAAIGGAITOAGTOGAGAIGITOITICIIG 542
                                                                                                                                                                                                                                                                                 sThrValAspArqAspThrValCysGlyCysArqLysAsnGlnTyrArqH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 Asnatythrvatnistonsorrysatnatniysatnasmihrvatrysma 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 743 ACTIGTAAGAAAAGCCTGGAAGTGCACGAAGTTGTGCCTACCCAGATTGAG 792
56 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCycArqGluC 73
                                                                                        73 ysdluSordlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 89
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/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tound through the I.M.A.G.E. Consortium/LENE at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://image.llnl.gov
Plate: LLAM10185 row: g column: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 AsnValiysGlyThrGluAspSerGlyThr 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   793 AATGTTAAGGGCACTGAGGACTCAGGCACCACA 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /orqanism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib-"NIH_MGC_91"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xrof-"taxon.9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cqapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              974
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/note-"Organ: prostate; Vector: pGMV-SPORT6; Site_1: Not1; Site_2: Salf, Cloned unidirectionally, olique dr primed. Average insert size 1.4 kb. Library enriched for full length clones and constructed by Life Ecchnologies. Note: this is a NIH_MOC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 TGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATGTCTTGTTGCAC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 GlyThrValHisLeuSerCySClnGluLySGlnAsnThrValCySThrCy 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 sHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerAsnC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               501 CCATGCAGGTTCTTTCTAAGAGAAAAGGAGTGTGTCCCTGTAGTAACT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 ystystysSerticuGlaCysThrLysLeuCysLeuProGlnfleGluAsn 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 CysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysTh 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 rValAspArgAspThrValCySGlyCysArgLysAsuGlnTyrArqHisT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 uTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluCysG 74
                                                                                                                                                                                                                                                                                                                                                                                                      2 GlyLeuSerThrValProAspLeuLeuProLeuValLeuGluLe 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 ProGlnAsnAsnSerIleCysCysThrLysCycHisLysGlyThrTyrLe 57
                                                                                                                                                                                                                                                                                                                                                                                                                            18 uLeuValGlyIleTyrProSerGl;ValIleGl;......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 luSerGlySerPheThrAlaSerGluAsnHisLeuArqHisCysLeuSer
                                                                                                                                                                                                                                                      Percent Similarity: 94.762 Percent Identity: 94.762
                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                      Gaps:
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US-09-525-998A-12 x BG180101
                                                                                                                                                                                                            Quality: 1112.50
Ratio: 5.590
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                                                                                                        259 a
                                                                                                                                                                                        alignment_scores.
                                                                                                      BASE COUNT
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa: Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eurheria: Primates; Catarrhini; Hominidae; Homo.
                                  AL522989 LT!_NFLOUY_NECT HOMO Sapiens cone CSODB009YP14 5
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BP 191 91006 EVRY cedex - France
Email: seqretigeEcos.ope.cus.lf, Web . www.genoscope.cns.lf.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li.W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type:"neuroblastoma_cells"
/lab_hest="nH10%"
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Genoscope - Centre National de Sequencage
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/sex-"male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Homo sapiens"
/db_xrof-"taxon-9606"
/clone-"CsOpponGYP14"
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1. .837
                                                                                                                                                                                         ALS22989.1 01.12786482
                                                                                                                    prime, mRNA sequence.
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US-09-525-998A-12 x AL522989
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                           AI.522989
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                                                                                                                                                                                                                                                                                        human.
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/clone="NTSEP300.6570"
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/cell_the="H12"
/cell_the="H1
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Mammaila; Eutheria; Primates; Catarrini; Hominidae; Homo.
[ (bases | to 76])
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Virology, Institute of Medical Science, University of Tokyo, and
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HRI human chNA project: 57: 8 17-chd one pass sequenting: Helix
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Yamamoto, J., Wakamatsu, A., Nakamura, Y., Naqai, I., Sugaro, S. and
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Tel: 81-428-52-3951
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162 TAGGGGACAGGGAGAAAAGAAGAAGAAGAAAATATATG 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 GOTCHTGGTGGGAATATAOOOOTGAGGGTATÜĞĞAOTGGTÇÇÇTÇAÇE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGAGATCTCTTGTTG 411
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                                                                                                                                                                                                                                                                                                                                                                                                                  40 HisproftaAsaAsaSortloCysCysThrtysCysHistysClyThrTy 56
                                                                                                                                                                                      1 MetGlyLeuSerThrValProAspLeuLeuLeuLeuValLeuLeuGl 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 Ser?ysSor'ys?ysArglysCluMetClyClulalClulloSerSerCy
                                                    Percent Similarity: 94.313 Percent Identity: 93.839
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                                                                                                                                                Align seg 1/1 to: AU141978 from: 1 to: 761
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                                                                                                            US-09-525-998A-12 x AUI31978
              Quality: 1107.50
Ratio: 5.565
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aliqnment_scores:
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AL577008 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1082YA01 5

prime, mRNA sequence. ALS77008 ALS77008.1 G1:12939716

mPNA

Seq_documentation_block: Locus AL577008

DEFINITION
ACCESSION
VERSION
KEYWORDS

16-PER 2001

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Actions "CSUDIO82YA01"

/clonel.bh=frI_MYLOGEPIL2"

/tissuc_type "placenta"

/note "Vector: pCMVSPORT 6; Site_1: Not!; lst strand cDNA

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mas primed with a Not! olidav(dT) primer. Five prime end

enriched, double stranded cDNA was digested with Not! I and

cloned into the Not! I and Eco RV sites of the pCMVSPORT 6
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                        Homo sapiens
Eukaryota: Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria, Primates, Catarihini, Hominidae; Homo.
11 (bases 1 to 975)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rockville, Maryland 20850, USA Fax : (1) 301-610-8371
Email : fliang@liletech.com URL :
http://lullength.invitrogen.com"
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BP 191-91006 EVRY cedex - France
Email: scyrefégenoscope ens.fr, Web - www.genoscope.cns.fr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 rteuTytAsnAspCysProGlyProGlyClnAspthrAspCysArqGluC 73
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                                                                                                                                                       Full-length cDNA libraries and normalization Unpublished (2001)
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Percent Identity: 92.417
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                                                                                                                                                                                                                                                                                                                                                                     /organism-"Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 c
                                                                                                                                                                                                                 Contact: Genoscope
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Furcent Similarity: 92.891
                                                                                                                                                                                                                                                                                                                                               . 975
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Align seq 1/1 to: AL529836 from: 1 to: 94z
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KEYWORDS
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//lab_host="neuroblastoma cells"
//lab_host="neuroblastoma cells"
//lab_host="neuroblastom"
//lab_host="neurobla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryola, Metacca, Chordata, Craniata, Vertebrata, Eulekeosteani,
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL529836 LTI_NFL001_NBC4 Homo sapiens cDNA clone C80DD005YP05 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HP 191 91006 FVRT codex - France
Email: segrefagenoscope.cns.fr. Web : www.genoscope.cns.fr.
                                                                         123 ioTyxTrpSerGluAonLeuPhaGludysPhaAsnCysSerLeuCysLeu 139
                                                                                                                                                                                                                                                                                        505 CACAGTGGACGGGGACACGTGTGTGCTGCAGGAAGAACCAGTACCGGC 655
                                                                                                                                                           656 ATTATIGGAGIGAAAACCITITCCAGIGCIICAATIGCAGCCICIGCCIC 705
                                                                                                                                                                                                                                         140 AsnGlyThrValHisLeuSerCysClnCluLysClnAsnThrValCysTh 156
                                                                                                                                                                                                                                                                                                                                                                                                        156 rCysHisAlaGlyPhePheLeuArqGluAsnGluCysValSerCysSerA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 sudystystysSerteuGludysThrtysten.CysteuProGlaffed 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 942)
Li,W.B., Gruber,C., Jessec,J. and Polayes,D.
Pull-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope - Centre National de Sequencage
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/clone_lib="LT1_NFL001_NBC4"
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/db_xrei-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 uAshValLysGlyThrGluAspSerGlyThr 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      856 GAAIGITAAGGCCACTGAGGAUTCAGGCACC 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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AL529836
AL529836.1 GI:12793329
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US-09-525-998A-12 x AL529836
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Eukaryota, Merazoa, Chordata, Cratiara, Vertebrata, Enteleostomi,
Mammalia, Extlectia, Pilhates, Carartilli, Hominidae, Homo.
1 (bases 1 to 845)
1 (bases 1 to 845)
2 (all Webinsons)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig. Websidenck of an exact the first factors. Fundamoto, i.e., Nakamura, Y., Nishikawa, T., Nagali, T., Sazaki, Y., Sagamo, S., and
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Lodds Anichosis 845 kp m.BNA EST 2003
LODD ANICHOR ANICHOSET NO. 2004 FOR A LODG THERMANNERS 5.7 BARRA
Sequence.
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                                                                                                         234 AFGGGCCTCT COACCTGCCT CACCTGCTGCTGCTGGTGTTCTTGTGGA 283
                                                                                                                                                                                                                                                                                                                                       284 GCTGTTGGTGGGAAATATACCCCTCAGGGGTAATTGGAGTGGTCGCCCACC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | FEFT | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 HisProGlaAsnAsnSerlleCysCysThrlysCysHisLysGlyThrT, 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56_rttentyrAsnAsp/ysProGtyProdty//thAspthrasp/ysArgGru/ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                ......AspserValCysProGinGryPysPylle 49
i MetolyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuSi
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Zeoll type="teratrovareinoma" // Zeoll time="nut" // Zeoll time="n
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HRI human cDNA project; 75. & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction. Department of Virology, Institute of Medical Science, University of Tokyo, and
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                                                                                                                                                                                                                                                                      1532-3 Yana, Kisaranu, Chiba 292 0812, Japan
Tel: 81-438-52 3951
Fax: 81-438-52-3952
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/db_xref-"taxon:9606"
/clone-"NT2RM4000896"
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                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genomics@hri.co.jp
HRI human cDNA project; 5'
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                                                                                                                                                                                                                                    Helix Research Institute
                                                                                                                                   Contact: Takao Isogai
Genomics Laboratory
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/note="Vector: pME188FL3; mRNA from uninduced NI2 neuronal precursor cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Uraniata, Vertebrata, Futeleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae; Homo. (Loss) 1.0.859. (Catarrhini, Hominidae; Homo. (La.). Wakannetsa,A. Gzawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Research Institute, CDMA library construction, Department of Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dmail: genomics@hri.co.jp
HRI human cDNA project; 57 & 3'-end one pass sequencing: Helix
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locus AU124446 859 bp mRNA EST
PFFINITION AU124446 NT28M4 Homo Sapicus CDNA close HIERM4000018 5', mRNA
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                                                                                                                140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 156
                                                                                        156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 173
                                                                                                                                                                                   173 snCystystysSericuGluCysThriysteuCysteuProGln11eGlu 189
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Tel: 81-438 52-3951
Fax: 81-438-52-3952
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/db_xref-"taxon:9606"
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Align seg 1/1 to: AU124446 from: 1 to: 859

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Eukaryota: Metaroa: Chordata: Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.
1 (bases 1 to 767)
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Naqai,T., Suqano,S. and
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1532-3 Yana, Kisaram, Chiba 292-9812, Japan
Tel: 81-488-52-3951
Fax: 81-488-52-3952
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602628106F1 NCL_CGAP_Skn4 Homo sapiens cDNA close IMAGE:4752912 57, /Lissue_Lype="squamous cell carcinoma" /lab.bust="bhilds (T) phage-resistant) /ncto "Organ skin Vertor powy-spope"s Site.1: Not1; Site.2: Sail; Cloned unidirectionally. Primer: Oligo dm. Average insert size 1.5kb. "ibrary constructed by infectionopies. Note: this is a NCI_CGAP Library." Eukaryota: Metazoa; Chordata, Craniala; Vertebrata; Euleleostomi; Tissue Producement: James Cleaver, M.D. cond. Library Preparation: life lechnologies, Inc. cond. Library Preparation: life lechnologies, Inc. Cond. Library Arrayed ky: The T M A G E Consoltium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Consoltium intormation can be Cloud through the L.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov NIH MCC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) 01-MAY-2001 Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo. 1 (bases 1 to 946) THEFTER THE THEFTER THE THEFTER THE THEFTER THE TRANSPORT TO SEE THE THE TRANSPORT TO SEE THE TRANSPORT TO SECURITIES TO SECURITIES TO SECURITIES TO SECURITIES TO SECURITIES THE TRANSPORT TO SECURITIES TOAspScrValCysProGlnGlyLysTyrIle 39 56 rLeuTyrAsnAspPysPr=GlyPr=GlyGluAspThrAspCysArgGluC 73 17 uLeuLeuValGlyIleTyrProSerGlyValIleGly..... Percent Identity: 87,440 Plate: LLAM10611 row: 1 column: 01 Length: /rlone_lib-"NCI_CGAP_Skn4" Align seq 1/1 to: PG681438 from: 1 to: 936 /organism-"Homo sapiens" Contact: Robert Strausberg, Ph.D. (-(-/clone-"IMAGE:4752912" /db_xrof-"taxon.gkök" Location/Qualifiers 1. .936 Email: cgapbs-r@mail.nih.gov mRNA 740 ACTGTAAGAAAAGCCTGGAATGCACN 765 High quality sequence stop. BG681438.1 G1:13912835 936 bp US-09-525-998A 12 x RG681438 Quality: 950.50 91.304 5.029 seq_name: ub_est2:RG681438 mENA sequence. BG681438 seq_documentation_block: Homo sapiens BG681438 Percent Similarity. Ratio: 30 human. alignment_scores: alignment block: S DEFINITION ORGANISM TITLE BASE COUNT ACCESSION REFERENCE AUTHORS KEYWORDS FEATURES VERSION COMMENT SOURCE ORIGIN

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site_E. Salr; Cloned unidirectionally. Primer: Oligo dr.
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/note="organ=lung; Vector=pCMV-SPORT6; Site,1: Not1;
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MCC clone distribution information can be
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1 (bases 1 to 971)
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http://image.llnl.gov
Plate: LLAM9674 row d column: 24
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Tissue Procurement: DCTD/DTF/Cazdar
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/clone="IMAGE:3890663"
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                                                                                                                           Quality: 946.50
Ratio: 5.035
Percent Similarity: 89.100
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                                      231 a
                                                                                                              alignment_scores:
                                                        ORIGIN
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LOCUS AU137990 772 Ep mRMA EST 25-007-2000 DEFINITION AU137950 PLACEL Homo sapiens cona clone PLACE1007638 5', mRNA

seq_documentation_block:

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Homo Sapiens
Bukatyola: Motazoa; Cherdata: Cianiata: Vertebrata: Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae: Homo.
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Man T. Nishikawatt. Stokity, Ishins. Salvo,K., Kawal,Y.,
Yamamoto,J., Nakamatsu,A., Nakamura,Y., Natai,T., Satado,S. and
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1542: Yana K Ksarazu, Chiba 292-1812, Japan
Itcl: 81 Att8-52-1951
Fax: 81 Att8-52-1952
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211 c 210 q 163
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/db_arel "taaon.9606"
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/tissuc_type="placenta"
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Aŭ137950.1 GI:10999511
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Unpublished (2000)
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Ratio: 5.325
Percent Similarity: 50.769
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Align seg 1/1 to: BE871809 from: 1 to: 969
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/clone="IMAGE-9875gs"
/clone=lih-"NIIIMGC_55"
/tissue_type="adenocarcinoms"
/tab_howt="DHIOH (phago-registant)"
/cote "Organ colon, Vertor pcMV Storie, Site_1, Noti,
/cote_2: Sali; cloned unidirectionally. Primer: Oligo dT.
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Eukaryota: Metasoa: Chordata, Craniata, Vertekrata, Euteleestemi;
Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
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601448388F1 NIH_MCC_65 Homo Sapiens cDNA clone IMAGE:3852525 5',
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Clone distribution: MGC clone distribution information can be
found through the L.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 969)
NIH-MGC http://mgc nci mih gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                491 AGCIGCICCAAATGCCAAAGGAAAIGAGICAGGIGGAGAICICIICIIG 540
                                           106 sThrValAspArgAspThrValCysCl7CysArgLysAshCln7yrArgH 123
                                                                                                                                  123 isTyrTrpSerGluAsnLeuPheGluCysPheAsnCysSerLeuCysLeu 139
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                                                                                                                                                                                                                                                                 641 AATGGGGACCGTGCAACTCTCCTGCCAGGAAACAGAACACAGAGGTGCAC 690
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/db_xrel="taxon:9606"
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Contact: Robert Strausberg, Ph D
Embil: cqapbs-rëmail.nih.qov
                                                                                                                                                                                                                                                                                                                                                                                                 173 AsnCys.LysLysSerLeuGluCysThrLys 182
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US-09-525-998A 12 x BE871809
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HRI human cDNA project (Ota.T., Wakamatsu, A., Ozawa, M., Ishii.S., Salto, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Naqai, T., Suzuki, Y., Sugano, S., Isogai, T.)
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Mammalla; Entheria; Primates; Catarrhini; Hominidae; Homo.
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
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1999S AUT25680 817 bp mPNA EST 23-OC1 2000
DEFINITION AUT25680 NT2FM4 Home sapiens chan clene NT2PM4092005 57, mRNA
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                                                                                                                                                                                                                                                                                                                             102 TACRGAAATATAHTIHTIHTIHTIHTIHTIHTIHTIHTIHTIHTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 gHisCysLeuSerCysSerLysCysArgLysGluMetGlyGlnValGlu1 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 leserSerCysThrValAspArgAspThrValCysGlyCysArgLysAsn 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 rLeuCysLeuAsnGlyThrValHisLeuSerCysClnClutysClnAsnT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 CCTCTCTCAATGGGACCGTGCACTCTCTCTCTGCTGGGAGAAACAGAAACA 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuAr 86
                                                                   2 AAATATATCCGCGCCTCAAAATAATTCGATTTGCTGTACAAGTGCCACA 51
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37 LysTyrileHis.ProClnAsnAsnSerileCysCysThrigsCysHist.
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1532 3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
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/note-"Vector: pME183FL3; mRNA from uninduced NT2 neuronal precursor cells" 4 6 238 c 231 g 182 t 4 others
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 SercysSerLysCycAraLycalaMetGlyclbValclulleSerSerCy 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             624 CACAGIGGACCGGGATACCGIGIGGGIGCAGGAAGAACCAGIACCGGC 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AspSerValCysProGlnGlyLysTyrIle 39
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                                                                                                                                                                                                                                                                                                                                                       5.485 Caps: 1
91,713 Percent (dentity: 90.608
                                                                                                                                                    /cell_type="teratocarcinoma"/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                        Length:
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                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ni2RM4002005"
/clone=lib="NT2RM4"
              Helix Mesearch Institute.
Location/Qualifiers
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US-09-525-998A-12 x AULL5680
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HG577121 929 Bp. HBMA ED ED ED ED ED ED ED MAY 2001 GGS2479211 HDT_GGAT_SKE4 HOMGO RAPIGER CHWA CH die IMAGE 4748614 51. HG677121 HG677121
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Mammalia: Eutberia: Primates; Catarrhini: Hominidae: Homo.
1 (bases 1-10-929)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.S.E. Consortion/LLNL at:
http://fonesells.poor.poor.b. column: 23
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Mathonal institutes of Health, Mahmualran Jene Follertion (MMC)
Unpublished (1999)
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Email: egaphs-remail.nih.gov
Tissue Provincement: James Cleaver, M.D.
cland library Preparation: Lite Lechaelouies, Inc.
cond. Library Arrayed by: The L.M.A.S.E. Consentiam (HANL)
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849	TCAGGGACTICAGG	٠.
198	183 eu.Cysleu.ProdinileGluAsnValLysGlyThrGluAspSerG	
662		
183	173Asn.CystysSert.cuCluCysThrtyst.	, -
749	700 GICACIGGAACCICIGCICCCAGAIICAAGCAAIICICCIGCIICAGCCI	
172	172	. 1
669	650 TAGAGRECTGCTCTGTCGCCCAGGCTFGGAATGCAGTGGCGCGATCTCGG (_
172	172 r	
649	600 ACCIGCOAIGCGIIICIIITCIAAGGAGAAAACGAGIGIGICICCIGIAG	-
172	GlyPhePheLeuArgCluAshGluCysValSerCysSe	
599	550 FCAATGGGACGTGCACCTCCCTGCCAGGAGAAACAGAAAACACGGTGGC	
155		
549		
139	122 qHisTyrTrpSerGluAsnLeuPheGlaCysPheAsnCysSerLeuCysL	
499	450 GPAPATAGAPPAGAPAPATATGTGTGTGTGTGTGTGTGTG	-
122		
449		-
106	89 uSerCysSorLysCysAraLysGluMetGlyGluValGlulleSerSerC	
366	350 TGTGAGAGGGGTGGTTGAGGGTTGAGAAAAGAGGGGTGAGAGAGTGGGTT	